

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: d'Apice, Anthony J.F.
Pearse, Martin J.
Robins, Allan J.
Crawford, Robert J.
Rathjen, Peter D.
- (ii) TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF
HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fish & Richardson
(B) STREET: 120 South Sixth Street, Suite 2500
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: USA
(F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30B
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/378,617
(B) FILING DATE: 26-JAN-1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ellinger, Mark S.
(B) REGISTRATION NUMBER: 34,812
(C) REFERENCE/DOCKET NUMBER: 06868/005001
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (612) 335-5070
(B) TELEFAX: (612) 288-9696

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGAATTCAG CCCTGCCTCC TTCTGCAG

28

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGAATTCAG GAGAAAATAA TGAATGTC

28

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGAATTCGG GATCTGCCTT GTACCACC

28

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGAATTCGA AATCACTGGG AATTTACA

28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGAATTCAG CATGATGCGC ATGAAGAC

28

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGAATTCT TTTTTTTTTT TVN

23

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCCCTGCCT CCTTCTGCAG AGCAGAGCTC ACTAGAACTT GTTTCGCCTT TTACTCTGGG 60

GGGAGAGAAG CAGAGGATGA GGAGAAAATA ATG AAT GTC AAA GGA AGA GTG GTT 114
 Met Asn Val Lys Gly Arg Val Val
 1 5

CTG TCA ATG CTG CTT GTC TCA ACT GTA ATG GTT GTG TTT TGG GAA TAC 162
 Leu Ser Met Leu Leu Val Ser Thr Val Met Val Val Phe Trp Glu Tyr
 10 15 20

ATC AAC AGC CCA GAA GGT TCT TTG TTC TGG ATA TAC CAG TCA AAA AAC 210
 Ile Asn Ser Pro Glu Gly Ser Leu Phe Trp Ile Tyr Gln Ser Lys Asn
 25 30 35 40

CCA GAA GTT GGC AGC AGT GCT CAG AGG GGC TGG TGG TTT CCG AGC TGG 258
 Pro Glu Val Gly Ser Ser Ala Gln Arg Gly Trp Trp Phe Pro Ser Trp
 45 50 55

TTT AAC AAT GGG ACT CAC AGT TAC CAC GAA GAA GAA GAC GCT ATA GGC 306
 Phe Asn Asn Gly Thr His Ser Tyr His Glu Glu Glu Asp Ala Ile Gly
 60 65 70

AAC GAA AAG GAA CAA AGA AAA GAA GAC AAC AGA GGA GAG CTT CCG CTA 354
 Asn Glu Lys Glu Gln Arg Lys Glu Asp Asn Arg Gly Glu Leu Pro Leu
 75 80 85

GTG GAC TGG TTT AAT CCT GAG AAA CGC CCA GAG GTC GTG ACC ATA ACC	402
Val Asp Trp Phe Asn Pro Glu Lys Arg Pro Glu Val Val Thr Ile Thr	
90 95 100	
AGA TGG AAG GCT CCA GTG GTA TGG GAA GGC ACT TAC AAC AGA GCC GTC	450
Arg Trp Lys Ala Pro Val Val Trp Glu Gly Thr Tyr Asn Arg Ala Val	
105 110 115 120	
TTA GAT AAT TAT TAT GCC AAA CAG AAA ATT ACC GTG GGC TTG ACG GTT	498
Leu Asp Asn Tyr Tyr Ala Lys Gln Lys Ile Thr Val Gly Leu Thr Val	
125 130 135	
TTT GCT GTC GGA AGA TAC ATT GAG CAT TAC TTG GAG GAG TTC TTA ATA	546
Phe Ala Val Gly Arg Tyr Ile Glu His Tyr Leu Glu Glu Phe Leu Ile	
140 145 150	
TCT GCA AAT ACA TAC TTC ATG GTT GGC CAC AAA GTC ATC TTT TAC ATC	594
Ser Ala Asn Thr Tyr Phe Met Val Gly His Lys Val Phe Tyr Ile	
155 160 165	
ATG GTG GAT GAT ATC TCC AGG ATG CCT TTG ATA GAG CTG GGT CCT CTG	642
Met Val Asp Asp Ile Ser Arg Met Pro Leu Ile Glu Leu Gly Pro Leu	
170 175 180	
CGT TCC TTT AAA GTG TTT GAG ATC AAG TCC GAG AAG AGG TGG CAA GAC	690
Arg Ser Phe Lys Val Phe Glu Ile Lys Ser Glu Lys Arg Trp Gln Asp	
185 190 195 200	
ATC AGC ATG ATG CGC ATG AAG ACC ATC GGG GAG CAC ATC CTG GCC CAC	738
Ile Ser Met Met Arg Met Lys Thr Ile Gly Glu His Ile Leu Ala His	
205 210 215	
ATC CAG CAC GAG GTG GAC TTC CTC TTC TGC ATG GAC GTG GAT CAG GTC	786
Ile Gln His Glu Val Asp Phe Leu Phe Cys Met Asp Val Asp Gln Val	
220 225 230	
TTC CAA AAC AAC TTT GGG GTG GAG ACC CTG GGC CAG TCG GTG GCT CAG	834
Phe Gln Asn Asn Phe Gly Val Glu Thr Leu Gly Gln Ser Val Ala Gln	
235 240 245	
CTA CAG GCC TGG TGG TAC AAG GCA CAT CCT GAC GAG TTC ACC TAC GAG	882
Leu Gln Ala Trp Trp Tyr Lys Ala His Pro Asp Glu Phe Thr Tyr Glu	
250 255 260	
AGG CGG AAG GAG TCC GCA GCC TAC ATT CCG TTT GGC CAG GGG GAT TTT	930
Arg Arg Lys Glu Ser Ala Ala Tyr Ile Pro Phe Gly Gln Gly Asp Phe	
265 270 275 280	
TAT TAC CAC GCA GCC ATT TTT GGG GGA ACA CCC ACT CAG GTT CTA AAC	978
Tyr Tyr His Ala Ala Ile Phe Gly Gly Thr Pro Thr Gln Val Leu Asn	
285 290 295	
ATC ACT CAG GAG TGC TTC AAG GGA ATC CTC CAG GAC AAG GAA AAT GAC	1026
Ile Thr Gln Glu Cys Phe Lys Gly Ile Leu Gln Asp Lys Glu Asn Asp	
300 305 310	
ATA GAA GCC GAG TGG CAT GAT GAA AGC CAT CTA AAC AAG TAT TTC CTT	1074
Ile Glu Ala Glu Trp His Asp Glu Ser His Leu Asn Lys Tyr Phe Leu	
315 320 325	

CTC AAC AAA CCC ACT AAA ATC TTA TCC CCA GAA TAC TGC TGG GAT TAT	1122
Leu Asn Lys Pro Thr Lys Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr	
330 335 340	
CAT ATA GGC ATG TCT GTG GAT ATT AGG ATT GTC AAG ATA GCT TGG CAG	1170
His Ile Gly Met Ser Val Asp Ile Arg Ile Val Lys Ile Ala Trp Gln	
345 350 355 360	
AAA AAA GAG TAT AAT TTG GTT AGA AAT AAC ATC T GACTTTAAAT	1214
Lys Lys Glu Tyr Asn Leu Val Arg Asn Asn Ile	
365 370	
TGTGCCAGCA GTTTTCTGAA TTIGAAAGAG TATTACTCTG GCTACTTCCT CAGAGAAGTA	1274
GCACCTTAATT TTAACCTTTTA AAAAAATACT AACAAAATAC CAACACAGTA AGTACATATT	1334
ATTCTTCCTT GCAACTTTGA GCCTTGTCAA ATGGGAGAAT GACTCTGTGG TAATCAGATG	1394
TAAATTCCCA GTGATTTC	1412

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGGGGGCGG GGCCGAGCTG GGAGCGTCGA GCCCGCTGCC CAGCGCCCGC CGGCTCCCTC	60
GCGCCCCTGC CCGCCGCCCC GGAGGAGCGC CCGGCGGCGG GCCGACGGGA GCGCAGCGGC	120
ACACCCCGCC CCGGCACGCC CGCGGGGCTC GGGAGGAGGC AGCGCGCCGA CTGTTCCGGC	180
AGCCGAGGAC GCCGCCGGGG AGCCGAGGCG CCGGCCAGCC CCCAGCGCGC CCAGCTTCTG	240
CGGATCAGGG AAACCACGTG TCCTCAAGTG GCCAGCCAGC TGTCCCAAG AGGAACTTGC	300
CTGGCATTTC CACGGAAAGA CGAGACACTT CACAAAATCA ACGGAGTCAG AAGGCTGCAC	360
CTTCGCTTCC TCCCAGCCCT GCCTCCTTCT GCAGAACGGA GCTCAGTAGA ACTTGGTACT	420
TTTGCCTTTT ACTCTAGGAG GAGAGAAGCA GACGATGAGG AGAAAATA ATG AAT GTC	477
Met Asn Val	
AAA GGA AAA GTG ATT CTG TCA ATG CTG GTT GTC TCA ACT GTC ATT GTT	525
Lys Gly Lys Val Ile Leu Ser Met Leu Val Val Ser Thr Val Ile Val	
5 10 15	
GTG TTT TGG GAA TAT ATC CAC AGC CCA GAA GGC TCT TTG TTC TGG ATA	573
Val Phe Trp Glu Tyr Ile His Ser Pro Glu Gly Ser Leu Phe Trp Ile	
20 25 30 35	
AAC CCA TCA AGA AAC CCA GAA GTT GGT GGC AGC AGC ATT CAG AAG GGC	621
Asn Pro Ser Arg Asn Pro Glu Val Gly Gly Ser Ser Ile Gln Lys Gly	
40 45 50	

TGG	TGG	CTT	CCG	AGA	TGG	TTT	AAC	AAT	GGT	TAC	CAT	GAA	GAA	GAT	GGA	669
Trp	Trp	Leu	Pro	Arg	Trp	Phe	Asn	Asn	Gly	Tyr	His	Glu	Glu	Asp	Gly	
			55					60					65			
GAC	ATA	AAC	GAA	GAA	AAG	GAA	CAA	AGA	AAC	GAA	GAC	GAA	AGC	AAG	CTT	717
Asp	Ile	Asn	Glu	Glu	Lys	Glu	Gln	Arg	Asn	Glu	Asp	Glu	Ser	Lys	Leu	
		70					75					80				
AAG	CTA	TCG	GAC	TGG	TTC	AAC	CCA	TTT	AAA	CGC	CCC	GAG	GTT	GTG	ACC	765
Lys	Leu	Ser	Asp	Trp	Phe	Asn	Pro	Phe	Lys	Arg	Pro	Glu	Val	Val	Thr	
	85					90					95					
ATG	ACG	AAG	TGG	AAG	GCT	CCA	GTG	GTG	TGG	GAA	GGC	ACT	TAC	AAC	AGA	813
Met	Thr	Lys	Trp	Lys	Ala	Pro	Val	Val	Trp	Glu	Gly	Thr	Tyr	Asn	Arg	
100					105					110					115	
GCC	GTC	TTA	GAC	AAT	TAT	TAT	GCC	AAG	CAG	AAA	ATT	ACC	GTC	GGC	CTG	861
Ala	Val	Leu	Asp	Asn	Tyr	Tyr	Ala	Lys	Gln	Lys	Ile	Thr	Val	Gly	Leu	
				120					125					130		
ACG	GTT	TTC	GCC	GTC	GGA	AGA	TAC	ATT	GAG	CAT	TAC	TTG	GAG	GAG	TTC	909
Thr	Val	Phe	Ala	Val	Gly	Arg	Tyr	Ile	Glu	His	Tyr	Leu	Glu	Glu	Phe	
			135				140						145			
TTA	ACG	TCT	GCT	AAT	AAG	CAC	TTC	ATG	GTG	GGC	CAC	CCA	GTC	ATC	TTT	957
Leu	Thr	Ser	Ala	Asn	Lys	His	Phe	Met	Val	Gly	His	Pro	Val	Ile	Phe	
		150					155					160				
TAT	ATC	ATG	GTA	GAT	GAT	GTC	TCC	AGG	ATG	CCT	TTG	ATA	GAG	TTG	GGT	1005
Tyr	Ile	Met	Val	Asp	Asp	Val	Ser	Arg	Met	Pro	Leu	Ile	Glu	Leu	Gly	
	165					170					175					
CCT	CTG	CGC	TCC	TTC	AAA	GTG	TTT	AAG	ATC	AAG	CCT	GAG	AAG	AGG	TGG	1053
Pro	Leu	Arg	Ser	Phe	Lys	Val	Phe	Lys	Ile	Lys	Pro	Glu	Lys	Arg	Trp	
180					185					190					195	
CAG	GAC	ATC	AGC	ATG	ATG	CGC	ATG	AAG	ACT	ATC	GGG	GAG	CAC	ATT	GTG	1101
Gln	Asp	Ile	Ser	Met	Met	Arg	Met	Lys	Thr	Ile	Gly	Glu	His	Ile	Val	
				200					205					210		
GCC	CAC	ATC	CAG	CAT	GAG	GTT	GAC	TTC	CTT	TTC	TGC	ATG	GAT	GTG	GAC	1149
Ala	His	Ile	Gln	His	Glu	Val	Asp	Phe	Leu	Phe	Cys	Met	Asp	Val	Asp	
			215					220					225			
CAG	GTC	TTC	CAA	GAC	AAG	TTT	GGG	GTG	GAG	ACC	CTG	GGC	GAG	TCG	GTG	1197
Gln	Val	Phe	Gln	Asp	Lys	Phe	Gly	Val	Glu	Thr	Leu	Gly	Glu	Ser	Val	
		230					235					240				
GCC	CAG	CTA	CAA	GCC	TGG	TGG	TAC	AAG	GCA	GAT	CCC	AAT	GAC	TTC	ACC	1245
Ala	Gln	Leu	Gln	Ala	Trp	Trp	Tyr	Lys	Ala	Asp	Pro	Asn	Asp	Phe	Thr	
	245					250					255					
TAC	GAG	AGG	CGG	AAG	GAG	TCT	GCA	GCA	TAC	ATT	CCC	TTC	GGC	GAA	GGG	1293
Tyr	Glu	Arg	Arg	Lys	Glu	Ser	Ala	Ala	Tyr	Ile	Pro	Phe	Gly	Glu	Gly	
260					265				270						275	
GAT	TTT	TAT	TAC	CAT	GCA	GCC	ATT	TTT	GGG	GGA	ACA	CCC	ACT	CAG	GTG	1341
Asp	Phe	Tyr	Tyr	His	Ala	Ala	Ile	Phe	Gly	Gly	Thr	Pro	Thr	Gln	Val	
				280					285					290		

CTT AAC ATC ACC CAG GAA TGC TTC AAA GGA ATC CTC AAG GAC AAG AAA	1389
Leu Asn Ile Thr Gln Glu Cys Phe Lys Gly Ile Leu Lys Asp Lys Lys	
295 300 305	
AAT GAC ATA GAA GCC CAA TGG CAT GAT GAA AGC CAT CTA AAC AAG TAT	1437
Asn Asp Ile Glu Ala Gln Trp His Asp Glu Ser His Leu Asn Lys Tyr	
310 315 320	
TTC CTT CTC AAC AAA CCT ACT AAA ATC TTA TCC CCG GAA TAC TGC TGG	1485
Phe Leu Leu Asn Lys Pro Thr Lys Ile Leu Ser Pro Glu Tyr Cys Trp	
325 330 335	
GAT TAT CAC ATA GGC CTA CCT GCG GAT ATT AAG CTT GTC AAG ATG TCT	1533
Asp Tyr His Ile Gly Leu Pro Ala Asp Ile Lys Leu Val Lys Met Ser	
340 345 350 355	
TGG CAG ACA AAA GAG TAT AAT GTG GTT AGA AAT AAT GTC T GACTTTGTGC	1583
Trp Gln Thr Lys Glu Tyr Asn Val Val Arg Asn Asn Val	
360 365	
CAGTACATTT CTGAATTTGA GAGAGTATTA TTCTGGCTAC TTCCTCAGAA AAGTAACACT	1643
TAATTTTAAC TTAAAAAAA ATACTAACAA AAGACCAACA CAGCAAATAC ATATTATTTT	1703
TCCTTGTAAC TTTGAGCCTT GTAATACGGG AGAATGAACC TGTGGTAATC AGATGTAAAT	1763
TCCAGTGAT TTCTTACCTA TTTTGGTTG TGGGGGCGGG GAATGGATAC ACCATCAGTT	1823
GAACC	1828

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGTCTTAGGA GGCTGGAGAT TCTGGGTGGA GCCCTAGCCC TGCCTTTTCT TAGCTGGCTG	60
ACACCTTCCC TTGTAGACTC TTCTTGGAAT GAGAAGTACC GATTCTGCTG AAGACCTCGC	120
GCTCTTAGGC TCTGGGAGTT GGAACCCTCG TACCTTCCTT TCCTCTGCTG AGCCCTGCCT	180
CCTTCGGCAG GCCAGAGCTG ACAGAAGCTC GGTGCTTTG CTGTTTGCTT TGGAGGGAAC	240
ACAGCTGACG ATGAGGCTGA CTTTGAATC AAGAGATCTG CTTACCCAG TCTCCTGGAA	300
TTAAAAGCCT GTACTACCTT GCCTGGACCT AAGATTTTCA TGATCACTAT GCTTCAAGAT	360
CTCCATGTCA ACAAGATCTC CATGTCAAGA TCCAAGTCAG AAACAAGTCT TCCATCCTCA	420
AGATCTGGAT CACAGGAGAA AATA ATG AAT GTC AAG GGA AAA GTA ATC CTG	471
Met Asn Val Lys Gly Lys Val Ile Leu	

TTG	ATG	CTG	ATT	GTC	TCA	ACC	GTG	GTT	GTC	GTG	TTT	TGG	GAA	TAT	GTC	519
Leu	Met	Leu	Ile	Val	Ser	Thr	Val	Val	Val	Val	Phe	Trp	Glu	Tyr	Val	
10					15					20					25	
AAC	AGC	CCA	GAC	GGC	TCT	TTC	TTG	TGG	ATA	TAT	CAC	ACA	AAA	ATT	CCA	567
Asn	Ser	Pro	Asp	Gly	Ser	Phe	Leu	Trp	Ile	Tyr	His	Thr	Lys	Ile	Pro	
				30					35					40		
GAG	GTT	GGT	GAG	AAC	AGA	TGG	CAG	AAG	GAC	TGG	TGG	TTC	CCA	AGC	TGG	615
Glu	Val	Gly	Glu	Asn	Arg	Trp	Gln	Lys	Asp	Trp	Trp	Phe	Pro	Ser	Trp	
			45					50					55			
TTT	AAA	AAT	GGG	ACC	CAC	AGT	TAT	CAA	GAA	GAC	AAC	GTA	GAA	GGA	CGG	663
Phe	Lys	Asn	Gly	Thr	His	Ser	Tyr	Gln	Glu	Asp	Asn	Val	Glu	Gly	Arg	
		60					65					70				
AGA	GAA	AAG	GGT	AGA	AAT	GGA	GAT	CGC	ATT	GAA	GAG	CCT	CAG	CTA	TGG	711
Arg	Glu	Lys	Gly	Arg	Asn	Gly	Asp	Arg	Ile	Glu	Glu	Pro	Gln	Leu	Trp	
	75					80					85					
GAC	TGG	TTC	AAT	CCA	AAG	AAC	CGC	CCG	GAT	GTT	TTG	ACA	GTG	ACC	CCG	759
Asp	Trp	Phe	Asn	Pro	Lys	Asn	Arg	Pro	Asp	Val	Leu	Thr	Val	Thr	Pro	
90					95					100					105	
TGG	AAG	GCG	CCG	ATT	GTG	TGG	GAA	GGC	ACT	TAT	GAC	ACA	GCT	CTG	CTG	807
Trp	Lys	Ala	Pro	Ile	Val	Trp	Glu	Gly	Thr	Tyr	Asp	Thr	Ala	Leu	Leu	
				110					115					120		
GAA	AAG	TAC	TAC	GCC	ACA	CAG	AAA	CTC	ACT	GTG	GGG	CTG	ACA	GTG	TTT	855
Glu	Lys	Tyr	Tyr	Ala	Thr	Gln	Lys	Leu	Thr	Val	Gly	Leu	Thr	Val	Phe	
			125					130					135			
GCT	GTG	GGA	AAG	TAC	ATT	GAG	CAT	TAC	TTA	GAA	GAC	TTT	CTG	GAG	TCT	903
Ala	Val	Gly	Lys	Tyr	Ile	Glu	His	Tyr	Leu	Glu	Asp	Phe	Leu	Glu	Ser	
		140					145					150				
GCT	GAC	ATG	TAC	TTC	ATG	GTT	GGC	CAT	CGG	GTC	ATA	TTT	TAC	GTC	ATG	951
Ala	Asp	Met	Tyr	Phe	Met	Val	Gly	His	Arg	Val	Ile	Phe	Tyr	Val	Met	
	155					160					165					
ATA	GAT	GAC	ACC	TCC	CGG	ATG	CCT	GTC	GTG	CAC	CTG	AAC	CCT	CTA	CAT	999
Ile	Asp	Asp	Thr	Ser	Arg	Met	Pro	Val	Val	His	Leu	Asn	Pro	Leu	His	
170					175					180					185	
TCC	TTA	CAA	GTC	TTT	GAG	ATC	AGG	TCT	GAG	AAG	AGG	TGG	CAG	GAT	ATC	1047
Ser	Leu	Gln	Val	Phe	Glu	Ile	Arg	Ser	Glu	Lys	Arg	Trp	Gln	Asp	Ile	
				190					195					200		
AGC	ATG	ATG	CGC	ATG	AAG	ACC	ATT	GGG	GAG	CAC	ATC	CTG	GCC	CAC	ATC	1095
Ser	Met	Met	Arg	Met	Lys	Thr	Ile	Gly	Glu	His	Ile	Leu	Ala	His	Ile	
			205					210					215			
CAG	CAC	GAG	GTC	GAC	TTC	CTC	TTC	TGC	ATG	GAC	GTG	GAT	CAA	GTC	TTT	1143
Gln	His	Glu	Val	Asp	Phe	Leu	Phe	Cys	Met	Asp	Val	Asp	Gln	Val	Phe	
			220				225					230				
CAA	GAC	AAC	TTC	GGG	GTG	GAA	ACT	CTG	GGC	CAG	CTG	GTA	GCA	CAG	CTC	1191
Gln	Asp	Asn	Phe	Gly	Val	Glu	Thr	Leu	Gly	Gln	Leu	Val	Ala	Gln	Leu	
	235					240					245					

CAG GCC TGG TGG TAC AAG GCC AGT CCC GAG AAG TTC ACC TAT GAG AGG Gln Ala Trp Trp Tyr Lys Ala Ser Pro Glu Lys Phe Thr Tyr Glu Arg 250 255 260 265	1239
CGG GAA CTG TCG GCC GCG TAC ATT CCA TTC GGA GAG GGG GAT TTT TAC Arg Glu Leu Ser Ala Ala Tyr Ile Pro Phe Gly Glu Gly Asp Phe Tyr 270 275 280	1287
TAC CAC GCG GCC ATT TTT GGA GGA ACG CCT ACT CAC ATT CTC AAC CTC Tyr His Ala Ala Ile Phe Gly Gly Thr Pro Thr His Ile Leu Asn Leu 285 290 295	1335
ACC AGG BAG TGC TTT AAG GGG ATC CTC CAG GAC AAG AAA CAT GAC ATA Thr Arg Glu Cys Phe Lys Gly Ile Leu Gln Asp Lys Lys His Asp Ile 300 305 310	1383
GAA GCC CAG TGG CAT GAT GAG AGC CAC CTC AAC AAA TAC TTC CTT TTC Glu Ala Gln Trp His Asp Glu Ser His Leu Asn Lys Tyr Phe Leu Phe 315 320 325	1431
AAC AAA CCC ACT AAA ATC CTA TCT CCA GAG TAT TGC TGG GAC TAT CAG Asn Lys Pro Thr Lys Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr Gln 330 335 340 345	1479
ATA GGC CTG CCT TCA GAT ATT AAA AGT GTC AAG GTA GCT TGG CAG ACA Ile Gly Leu Pro Ser Asp Ile Lys Ser Val Lys Val Ala Trp Gln Thr 350 355 360	1527
AAA GAG TAT AAT TTG GTT AGA AAT AAT GTC T GACTTCAAAT TGTGATGGAA Lys Glu Tyr Asn Leu Val Arg Asn Asn Val 365 370	1578
ACTTGACACT ATTACTCTGG CTAATTCCTC AAACAAGTAG CAACACTTGA TTTCAACTTT	1638
TAAAAGAAAC AATCAAAACC AAAACCCACT ACCATGGCAA ACAGATGATT TCTCCTGACA	1698
CCTTGAGCCT GTAATATGTG AGAAAGAGTC TATGGCAAGT AATCAGGTAT AAATTCTCAA	1758
TGATTTCTTA TATATTCTGG GTCTTGGGAA AACTTGATTC TAGAAATCAA AATTAATTTG	1818
ACAAAGGAAA AGCAGATGCC GGAACTTCT TCCCAGTCTG TCATACAATT CACCACTGGC	1878
CAGGTGCTGA GAGAAGCATT AGGGAACAGT GTGGGTGTG TCAGAGTTGG ACGGCTCCAT	1938
CCCTTTGGCT TCATTATCTT CCTCCTCATG GAGATTCTAA AGCAACCCAG AGAGGCTTTG	1998
CAGCCAGAGA CCTTTAATAA GGATGCCAAT GTGACCATCA GTCTGTAAAA GCTGATGGCT	2058
CCAGGAGCGC TGGCAGTCCA GGCCCCACTA GGCTATTGTT TCTGTCCTGG GCATAAAGGA	2118
GGCAGAGAGT GCCAATAGGT ACTTTGGTGG CACATGTTCA GAGTCCAGGA AAAATCAAGG	2178
GTGACCACTT AGAGGGACAT AGGACTTGGG GTTGGTGATT GAACTGAGTT ACAAACACAG	2238
ACAGCTTTCT TCAGGATGAC TAACAGCAGG AATTGAATGG AAAGTGTGTT CATTTTGTTT	2298
TGCCCCAATT GTATTCATGC TGTTAGCTTT GTGTGTTGAG CCCTGTGGAG AGGGTGTGAC	2358
TGTATCAGGG AAGGAGAGTA CCTCAGCGGA CTGAGGACCA GCACCCTATT ATATCAGAAG	2418
ACAATCTCTC ATCATCAGGT CCTACCTACA ACCTGCTCTG AACCTCCGAG TTCCTCAGCC	2478

CATCGTGTTC CAGTGTGGGG GCCTGTATGG AGCAGGTGAC TGAAGACAAA GCCCCCTGTC 2538
 ACATGACCTC ATTTCCCCTG CTCTAGTACT ATGCAAGTGT GACAGCCAGC CAGCCAGATG 2598
 TACTGGACAA CATAGGAACC GACTTTATGG CAATGGGAGC CGCAGTCACT ACAACGGAGC 2658
 TGCTGAAGGT TCTGTTCCCC GCTCTGAGAG CCTGCAGGAG CCCCTGTATA GGTGGTTCTC 2718
 AACCTATGGG TCGCGACCCC TTTGGGAAGT GTTAAATGAC CCTTTCACAG GTGTCCCCTA 2778
 AGACGGTTAA AAAACATAGA TATTTCCACT CTGACTGGTA ACAGTAGCAG AATTACAGTT 2838
 ATGAAATAGC AAGGGAAATA ATTCTGGGGT TCGTGTCAAT CATAACCATGA GGAGCTACAT 2898
 TAGGTCACAT CATTAGGGAA GTTGAGAAGC ATAGCTCTAC TTGGGTATTT AAGCAAATTA 2958
 TGCAAAGGGG GTTGTCGCTC TGTGTTCTGT GTATGCATAT ATTTATATTT TGCTTGTCTT 3018
 CCAGTTTAGG TCAATCTGTT TCTTCCTTA AGCAGTTTAT TTAAAAGGCC ATTGCACCAT 3078
 CTTGGTGAAC AGCATGAGGG GTTTCAATAA AAAATAGGAT CTTACCTTTG TCCACAGGGC 3138
 TCTACCTCTT ACTTTTCAAT TGTGAACAAA AAAGGTCGCA CACCCAGAGG CAACAAAACC 3198
 CACAGAATTC CTGAACCAAT GGGAGATGCC AATGGAAGCA GAGCTGCAC ATCTGCTAAA 3258
 AATTCTGCCT CTCTGTCACT GTGCTGGATC CGTCTAAAGT GGGACAGTTC AATGGTCTGA 3318
 AAGTTTCAA AAGGCTGGGG AATTTGAGGG GATTTTTTTT TAAAATAAAA TTGATCCAAG 3378
 TTTAAATCTC TAATGAGTAA GCTTAGGATT TTATTAAAGG TAATTTTATG ACATTCTTCA 3438
 AAATAAGAAT TC 3450

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asn Val Lys Gly Arg Val Val Leu Ser Met Leu Leu Val Ser Thr
 1 5 10 15
 Val Met Val Val Phe Trp Glu Tyr Ile Asn Ser Pro Glu Gly Ser Leu
 20 25 30
 Phe Trp Ile Tyr Gln Ser Lys Asn Pro Glu Val Gly Ser Ser Ala Gln
 35 40 45
 Arg Gly Trp Trp Phe Pro Ser Trp Phe Asn Asn Gly Thr His Ser Tyr
 50 55 60
 His Glu Glu Glu Asp Ala Ile Gly Asn Glu Lys Glu Gln Arg Lys Glu
 65 70 75 80
 Asp Asn Arg Gly Glu Leu Pro Leu Val Asp Trp Phe Asn Pro Glu Lys
 85 90 95

Arg Pro Glu Val Val Thr Ile Thr Arg Trp Lys Ala Pro Val Val Trp
 100 105 110
 Glu Gly Thr Tyr Asn Arg Ala Val Leu Asp Asn Tyr Tyr Ala Lys Gln
 115 120 125
 Lys Ile Thr Val Gly Leu Thr Val Phe Ala Val Gly Arg Tyr Ile Glu
 130 135 140
 His Tyr Leu Glu Glu Phe Leu Ile Ser Ala Asn Thr Tyr Phe Met Val
 145 150 155 160
 Gly His Lys Val Ile Phe Tyr Ile Met Val Asp Asp Ile Ser Arg Met
 165 170 175
 Pro Leu Ile Glu Leu Gly Pro Leu Arg Ser Phe Lys Val Phe Glu Ile
 180 185 190
 Lys Ser Glu Lys Arg Trp Gln Asp Ile Ser Met Met Arg Met Lys Thr
 195 200 205
 Ile Gly Glu His Ile Leu Ala His Ile Gln His Glu Val Asp Phe Leu
 210 215 220
 Phe Cys Met Asp Val Asp Gln Val Phe Gln Asn Asn Phe Gly Val Glu
 225 230 235 240
 Thr Leu Gly Gln Ser Val Ala Gln Leu Gln Ala Trp Trp Tyr Lys Ala
 245 250 255
 His Pro Asp Glu Phe Thr Tyr Glu Arg Arg Lys Glu Ser Ala Ala Tyr
 260 265 270
 Ile Pro Phe Gly Gln Gly Asp Phe Tyr Tyr His Ala Ala Ile Phe Gly
 275 280 285
 Gly Thr Pro Thr Gln Val Leu Asn Ile Thr Gln Glu Cys Phe Lys Gly
 290 295 300
 Ile Leu Gln Asp Lys Glu Asn Asp Ile Glu Ala Glu Trp His Asp Glu
 305 310 315 320
 Ser His Leu Asn Lys Tyr Phe Leu Leu Asn Lys Pro Thr Lys Ile Leu
 325 330 335
 Ser Pro Glu Tyr Cys Trp Asp Tyr His Ile Gly Met Ser Val Asp Ile
 340 345 350
 Arg Ile Val Lys Ile Ala Trp Gln Lys Lys Glu Tyr Asn Leu Val Arg
 355 360 365
 Asn Asn Ile
 370

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Asn	Val	Lys	Gly	Lys	Val	Ile	Leu	Ser	Met	Leu	Val	Val	Ser	Thr	1	5	10	15
Val	Ile	Val	Val	Phe	Trp	Glu	Tyr	Ile	His	Ser	Pro	Glu	Gly	Ser	Leu	20	25	30	
Phe	Trp	Ile	Asn	Pro	Ser	Arg	Asn	Pro	Glu	Val	Gly	Gly	Ser	Ser	Ile	35	40	45	
Gln	Lys	Gly	Trp	Trp	Leu	Pro	Arg	Trp	Phe	Asn	Asn	Gly	Tyr	His	Glu	50	55	60	
Glu	Asp	Gly	Asp	Ile	Asn	Glu	Glu	Lys	Glu	Gln	Arg	Asn	Glu	Asp	Glu	65	70	75	80
Ser	Lys	Leu	Lys	Leu	Ser	Asp	Trp	Phe	Asn	Pro	Phe	Lys	Arg	Pro	Glu	85	90	95	
Val	Val	Thr	Met	Thr	Lys	Trp	Lys	Ala	Pro	Val	Val	Trp	Glu	Gly	Thr	100	105	110	
Tyr	Asn	Arg	Ala	Val	Leu	Asp	Asn	Tyr	Tyr	Ala	Lys	Gln	Lys	Ile	Thr	115	120	125	
Val	Gly	Leu	Thr	Val	Phe	Ala	Val	Gly	Arg	Tyr	Ile	Glu	His	Tyr	Leu	130	135	140	
Glu	Glu	Phe	Leu	Thr	Ser	Ala	Asn	Lys	His	Phe	Met	Val	Gly	His	Pro	145	150	155	160
Val	Ile	Phe	Tyr	Ile	Met	Val	Asp	Asp	Val	Ser	Arg	Met	Pro	Leu	Ile	165	170	175	
Glu	Leu	Gly	Pro	Leu	Arg	Ser	Phe	Lys	Val	Phe	Lys	Ile	Lys	Pro	Glu	180	185	190	
Lys	Arg	Trp	Gln	Asp	Ile	Ser	Met	Met	Arg	Met	Lys	Thr	Ile	Gly	Glu	195	200	205	
His	Ile	Val	Ala	His	Ile	Gln	His	Glu	Val	Asp	Phe	Leu	Phe	Cys	Met	210	215	220	
Asp	Val	Asp	Gln	Val	Phe	Gln	Asp	Lys	Phe	Gly	Val	Glu	Thr	Leu	Gly	225	230	235	240
Glu	Ser	Val	Ala	Gln	Leu	Gln	Ala	Trp	Trp	Tyr	Lys	Ala	Asp	Pro	Asn	245	250	255	
Asp	Phe	Thr	Tyr	Glu	Arg	Arg	Lys	Glu	Ser	Ala	Ala	Tyr	Ile	Pro	Phe	260	265	270	
Gly	Glu	Gly	Asp	Phe	Tyr	Tyr	His	Ala	Ala	Ile	Phe	Gly	Gly	Thr	Pro	275	280	285	
Thr	Gln	Val	Leu	Asn	Ile	Thr	Gln	Glu	Cys	Phe	Lys	Gly	Ile	Leu	Lys	290	295	300	
Asp	Lys	Lys	Asn	Asp	Ile	Glu	Ala	Gln	Trp	His	Asp	Glu	Ser	His	Leu	305	310	315	320

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met 1	Asn	Val	Lys	Gly 5	Lys	Val	Ile	Leu	Leu 10	Met	Leu	Ile	Val	Ser 15	Thr
Val	Val	Val	Val 20	Phe	Trp	Glu	Tyr	Val 25	Asn	Ser	Pro	Asp	Gly 30	Ser	Phe
Leu	Trp	Ile 35	Tyr	His	Thr	Lys	Ile 40	Pro	Glu	Val	Gly	Glu 45	Asn	Arg	Trp
Gln	Lys 50	Asp	Trp	Trp	Phe	Pro 55	Ser	Trp	Phe	Lys	Asn 60	Gly	Thr	His	Ser
Tyr 65	Gln	Glu	Asp	Asn 70	Val	Glu	Gly	Arg	Arg	Glu 75	Lys	Gly	Arg	Asn	Gly 80
Asp	Arg	Ile	Glu	Glu 85	Pro	Gln	Leu	Trp	Asp 90	Trp	Phe	Asn	Pro	Lys 95	Asn
Arg	Pro	Asp	Val 100	Leu	Thr	Val	Thr	Pro 105	Trp	Lys	Ala	Pro	Ile 110	Val	Trp
Glu	Gly	Thr 115	Tyr	Asp	Thr	Ala	Leu 120	Leu	Glu	Lys	Tyr	Tyr 125	Ala	Thr	Gln
Lys	Leu 130	Thr	Val	Gly	Leu	Thr 135	Val	Phe	Ala	Val	Gly 140	Lys	Tyr	Ile	Glu
His 145	Tyr	Leu	Glu	Asp	Phe 150	Leu	Glu	Ser	Ala	Asp 155	Met	Tyr	Phe	Met	Val 160
Gly	His	Arg	Val	Ile 165	Phe	Tyr	Val	Met	Ile 170	Asp	Asp	Thr	Ser	Arg 175	Met
Pro	Val	Val	His 180	Leu	Asn	Pro	Leu	His 185	Ser	Leu	Gln	Val	Phe 190	Glu	Ile
Arg	Ser	Glu 195	Lys	Arg	Trp	Gln	Asp 200	Ile	Ser	Met	Met	Arg 205	Met	Lys	Thr
Ile	Gly 210	Glu	His	Ile	Leu	Ala 215	His	Ile	Gln	His	Glu 220	Val	Asp	Phe	Leu

Phe Cys Met Asp Val Asp Gln Val Phe Gln Asp Asn Phe Gly Val Glu
 225 230 235 240
 Thr Leu Gly Gln Leu Val Ala Gln Leu Gln Ala Trp Trp Tyr Lys Ala
 245 250 255
 Ser Pro Glu Lys Phe Thr Tyr Glu Arg Arg Glu Leu Ser Ala Ala Tyr
 260 265 270
 Ile Pro Phe Gly Glu Gly Asp Phe Tyr Tyr His Ala Ala Ile Phe Gly
 275 280 285
 Gly Thr Pro Thr His Ile Leu Asn Leu Thr Arg Glu Cys Phe Lys Gly
 290 295 300
 Ile Leu Gln Asp Lys Lys His Asp Ile Glu Ala Gln Trp His Asp Glu
 305 310 315 320
 Ser His Leu Asn Lys Tyr Phe Leu Phe Asn Lys Pro Thr Lys Ile Leu
 325 330 335
 Ser Pro Glu Tyr Cys Trp Asp Tyr Gln Ile Gly Leu Pro Ser Asp Ile
 340 345 350
 Lys Ser Val Lys Val Ala Trp Gln Thr Lys Glu Tyr Asn Leu Val Arg
 355 360 365
 Asn Asn Val
 370

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGGGCTGCA GGAATTCGAT GATCCCCCAG CTTGAAGTTC CTATTCCGAA GTTCCTATTC	60
TCTAGAAAGT ATAGGAACTT GAAGCTGGGC TGCAGGAATT CGATTGAGC AGTGTGGTTT	120
TGCAAGAGGA AGCAAAAAGC CTCTCCACCC AGGCCTGGAA TGTTTCCACC CAATGTCGAG	180
CAGTGTGGTT TTGCAAGAGG AAGCAAAAAG CCTCTCCACC CAGGCCTGGA ATGTTTCCAC	240
CCAATGTCGA GCAAACCCCG CCCAGCGTCT TGTCATTGGC GAATTCGAAC ACGCAGATGC	300
AGTCGGGGCG GCGCGGTCCC AGGTCCACTT GGCATATTAA GGTGACGCGT GTGGCCTCGA	360
ACACCGAGCG ACCCTGCAGC CAATATGGGA TCGGCCATTG AACAAGATGG ATTGCACGCA	420
GGTTCTCCGG CCGCTTGGGT GGAGAGGCTA TTCGGCTATG ACTGGGCACA ACAGACAATC	480
GGCTGCTCTG ATGCCGCCGT GTTCCGGCTG TCAGCGCAGG GGCGCCCGGT TCTTTTGTG	540

AAGACCGACC TGTCCGGTGC CCTGAATGAA CTCCAAGACG AGGCAGCGCG GCTATCGTGG	600
CTGGCCACGA CGGGCGTTCC TTGCGCAGCT GTGCTCGACG TTGTCACTGA TGCGGGAAGG	660
GACTGGCTGC TATTGGGCGA AGTGCCGGGG CAGGATCTCC TGTCACTCA CCTTGCTCCT	720
GCCGAGAAAG TATCCATCAT GGCTGATGCA ATGCGGCGGC TGCATACGCT TGATCCGCT	780
ACCTGCCCCAT TCGACCACCA AGCGAAACAT CGCATCGAGC GAGCACGTAC TCGGATGGAA	840
GCCGGTCTTG TCGATCAGGA TGATCTGGAC GAAGAGCATC AGGGGCTCGC GCCAGCC3AA	900
CTGTTGCGCA GGCTCAAGGC GCGGATGCCC GACGGCGAGG ATCTCTCGT GACCCATGGC	960
GATGCCTGCT TGCCGAATAT CATGGTGGAA AATGGCCGCT TTTCTGGATT CATCGACTGT	1020
GGCCGGCTGG GTGTGGCGGA CCGCTATCAG GACATAGCGT TGGCTACCCG TGATATTGCT	1080
GAAGAGCTTG GCGGCGAATG GGCTGACCGC TTCCTCGTGC TTTACGGTAT CGCCGCTCCC	1140
GATTGCGAGC GCATCGCCTT CTATCGCCTT CTTGACGAGT TCTTCTGAGG GGATCGGCAA	1200
TAAAAGACA GAATAAACG CACGGGTGTT GGGCGTTTGT TCGGATCATC AAGCTTGAAG	1260
TTCCTATTCC GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTCAAGCTT ATCGATGAGT	1320
AGATCTTGAT CGATACCGTC	1340

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTGGAAAA GTACTACGCC ACACAGAAAC TCA

33

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCCAGAGTA ATAGTGTCAG GTTCCATCA CAA

33

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCACACGCG TCACCTTAAT AATATGCCAA GTGGAC

36

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCAGCATGAT GCGCATGAAG AC

22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGCCGCGTG GTAGTAAAAA

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCTTGACGAG TTCTTCTGAG

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGAGATCGC ATTGAAGAGC

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGGCCGCGTG GTAGTAAAAA

20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGGTTTTTGGT TTTGATTGTT

20

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGAATTCAT GTTAAACATG GGAGGCCCC

29

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGAATTCTG CCCACTCCCT GCCGATG

27

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 714 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTGACACCTT TCGCTTTCCT CTGCGTGTG CGCCTGCGAC CTTTCCCCAC CCCGGCCTCT	60
TTCCTGGTTG CACCACTTCC TCTCATTCCA AAGGATTGTG CCCTTACTGC TGCTGGTTCT	120
GCACTGGAAG CACGGGGCAG GGAGCCCTCT TCCCATCACC CCTGTAAATG CCACCTGTGC	180
CATACGCCAC CCATGCCACG GCAACCTC ATG AAC CAG ATC AAG AAT CAA CTG	232
Met Asn Gln Ile Lys Asn Gln Leu	375
GCA CAG CTC AAT GGC AGC GCC AAT GCT CTC TTC ATT TCC TAT TAC ACA	280
Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe Ile Ser Tyr Tyr Thr	380 385 390 395
GCT CAA GGG GAG CCG TTT CCC AAC AAC GTG GAA AAG CTA TGT GCG CCT	328
Ala Gln Gly Glu Pro Phe Pro Asn Asn Val Glu Lys Leu Cys Ala Pro	400 405 410
AAC ATG ACA GAC TTC CCA TCT TTC CAT GGC AAC GGG ACA GAG AAG ACC	376
Asn Met Thr Asp Phe Pro Ser Phe His Gly Asn Gly Thr Glu Lys Thr	415 420 425

AAG TTG GTG GAG CTG TAT CGG ATG GTC GCA TAC CTG AGC GCC TCC CTG	424
Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr Leu Ser Ala Ser Leu	
430 435 440	
ACC AAT ATC ACC CGG GAC CAG AAG GTC CTG AAC CCC ACT GCC GTG AGC	472
Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn Pro Thr Ala Val Ser	
445 450 455	
CTC CAG GTC AAG CTC AAT GCT ACT ATA GAC GTC ATG AGG GGC CTC CTC	520
Leu Gln Val Lys Leu Asn Ala Thr Ile Asp Val Met Arg Gly Leu Leu	
460 465 470 475	
AGC AAT GTG CTT TGC CGT CTG TGC AAC AAG TAC CGT GTG GGC CAC GTG	568
Ser Asn Val Leu Cys Arg Leu Cys Asn Lys Tyr Arg Val Gly His Val	
480 485 490	
GAT GTG CCA CCT GTC CCC GAC CAC TCT GAC AAA GAA GCC TTC CAA AGG	616
Asp Val Pro Val Pro Asp His Ser Asp Lys Glu Ala Phe Gln Arg	
495 500 505	
AAA AAG TTG GGT TGC CAG CTT CTG GGG ACA TAC AAG CAA GTC ATA AGT	664
Lys Lys Leu Gly Cys Gln Leu Leu Gly Thr Tyr Lys Gln Val Ile Ser	
510 515 520	
GTG GTG GTC CAG GCC TTC T AGAGAGGAGG TCTTGAATGT ACCATGGACT	713
Val Val Val Gln Ala Phe	
525	

G

714

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Asn Gln Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn	1 5 10 15
Ala Leu Phe Ile Ser Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn	20 25 30
Asn Val Glu Lys Leu Cys Ala Pro Asn Met Thr Asp Phe Pro Ser Phe	35 40 45
His Gly Asn Gly Thr Glu Lys Thr Lys Leu Val Glu Leu Tyr Arg Met	50 55 60
Val Ala Tyr Leu Ser Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys	65 70 75 80
Val Leu Asn Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr	85 90 95

153

Ile. Asp Val Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys
100 105 110
Asn Lys Tyr Arg Val Gly His Val Asp Val Pro Pro Val Pro Asp His
115 120 125
Ser Asp Lys Glu Ala Phe Gln Arg Lys Lys Leu Gly Cys Gln Leu Leu
130 135 140
Gly Thr Tyr Lys Gln Val Ile Ser Val Val Val Gln Ala Phe
145 150 155

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACACGGTACT TGTGCA

17

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTCTGGTCCC GGGTGATATT GGTCA

25

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCATGGCCTC GAGGGCCCCC CCCCCCCC

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CACCTTTCGC TTTCCT

16

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACCTTTTGC CTTTTCTCTC TCCTGGTGCA CCATTTCTC TCCCTCCCTG AGCCGGAGTT	60
GTGCCCCCTGC TGTGGTTCT GCACTGGAAA CATGGGGCGG GGAGCCCCCT CCCCATCACC	120
CCTGTCAACG CCACCTGTGC CATACGCCAC CCATGTCACA ACAACCTC ATG AAC CAG	177
	Met Asn Gln
	160
ATC AGG AGC CAA CTG GCA CAG CTC AAT GGC AGT GCC AAT GCC CTC TTT	225
Ile Arg Ser Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe	
	165 170 175
ATT CTC TAT TAC ACA GCC CAG GGG GAG CCG TTC CCC AAC AAC CTG GAC	273
Ile Leu Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Leu Asp	
	180 185 190
AAG CTA TGT GGC CCC AAC GTG ACG GAC TTC CCG CCC TTC CAC GCC AAC	321
Lys Leu Cys Gly Pro Asn Val Thr Asp Phe Pro Pro Phe His Ala Asn	
	195 200 205
GGC ACG GAG AAG GCC AAG CTG GTG GAG CTG TAC CGC ATA GTC GTG TAC	369
Gly Thr Glu Lys Ala Lys Leu Val Glu Leu Tyr Arg Ile Val Val Tyr	
	210 215 220 225
CTT GGC ACC TCC CTG GGC AAC ATC ACC CGG GAC CAG AAG ATC CTC AAC	417
Leu Gly Thr Ser Leu Gly Asn Ile Thr Arg Asp Gln Lys Ile Leu Asn	
	230 235 240
CCC AGT GCC CTC AGC CTC CAC AGC AAG CTC AAC GCC ACC GCC GAC ATC	465
Pro Ser Ala Leu Ser Leu His Ser Lys Leu Asn Ala Thr Ala Asp Ile	
	245 250 255
CTG CGA GGC CTC CTT AGC AAC GTG CTG TGC CGC CTG TGC AGC AAG TAC	513
Leu Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Ser Lys Tyr	
	260 265 270

CAC GTG GGC CAT GTG GAC GTG ACC TAC GGC CCT GAC ACC TCG GGT AAG 561
 His Val Gly His Val Asp Val Thr Tyr Gly Pro Asp Thr Ser Gly Lys
 275 280 285
 GAT GTC TTC CAG AAG AAG AAG CTG GGC TGT CAA CTC CTG GGG AAG TAT 609
 Asp Val Phe Gln Lys Lys Lys Leu Gly Cys Gln Leu Leu Gly Lys Tyr
 290 295 300 305
 AAG CAG ATC ATC GCC GTG TTG GCC CAG GCC TTC T AGCAGGAGGT 653
 Lys Gln Ile Ile Ala Val Leu Ala Gln Ala Phe
 310 315
 CT 655

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Asn Gln Ile Arg Ser Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn
 1 5 10 15
 Ala Leu Phe Ile Leu Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn
 20 25 30
 Asn Leu Asp Lys Leu Cys Gly Pro Asn Val Thr Asp Phe Pro Pro Phe
 35 40 45
 His Ala Asn Gly Thr Glu Lys Ala Lys Leu Val Glu Leu Tyr Arg Ile
 50 55 60
 Val Val Tyr Leu Gly Thr Ser Leu Gly Asn Ile Thr Arg Asp Gln Lys
 65 70 75 80
 Ile Leu Asn Pro Ser Ala Leu Ser Leu His Ser Lys Leu Asn Ala Thr
 85 90 95
 Ala Asp Ile Leu Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys
 100 105 110
 Ser Lys Tyr His Val Gly His Val Asp Val Thr Tyr Gly Pro Asp Thr
 115 120 125
 Ser Gly Lys Asp Val Phe Gln Lys Lys Lys Leu Gly Cys Gln Leu Leu
 130 135 140
 Gly Lys Tyr Lys Gln Ile Ile Ala Val Leu Ala Gln Ala Phe
 145 150 155

(2). INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGTTGGTTC TGCACTGGA